1/24

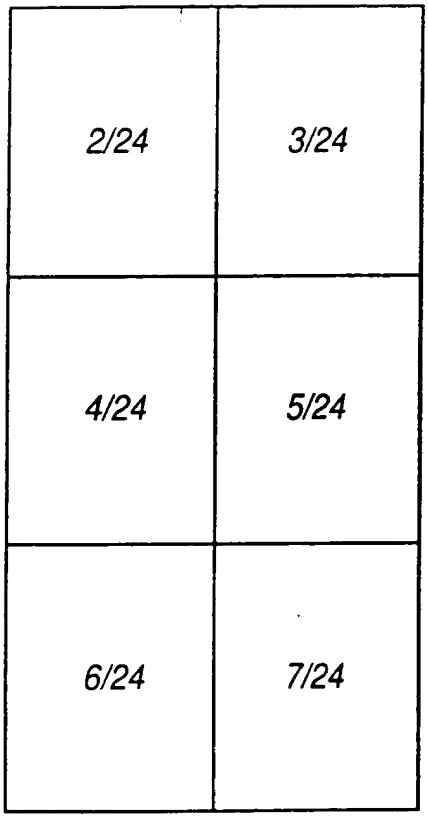


Fig. 1

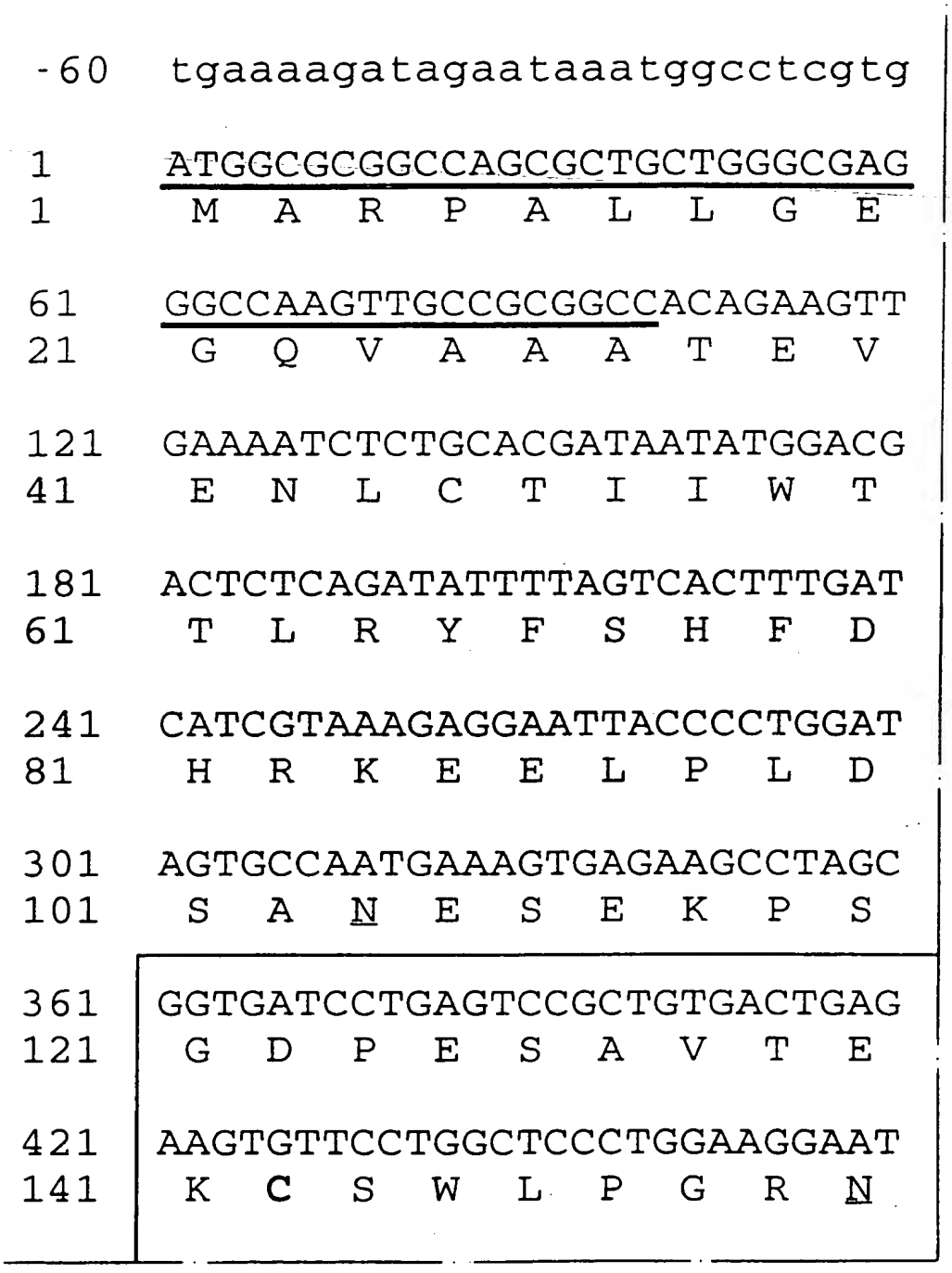
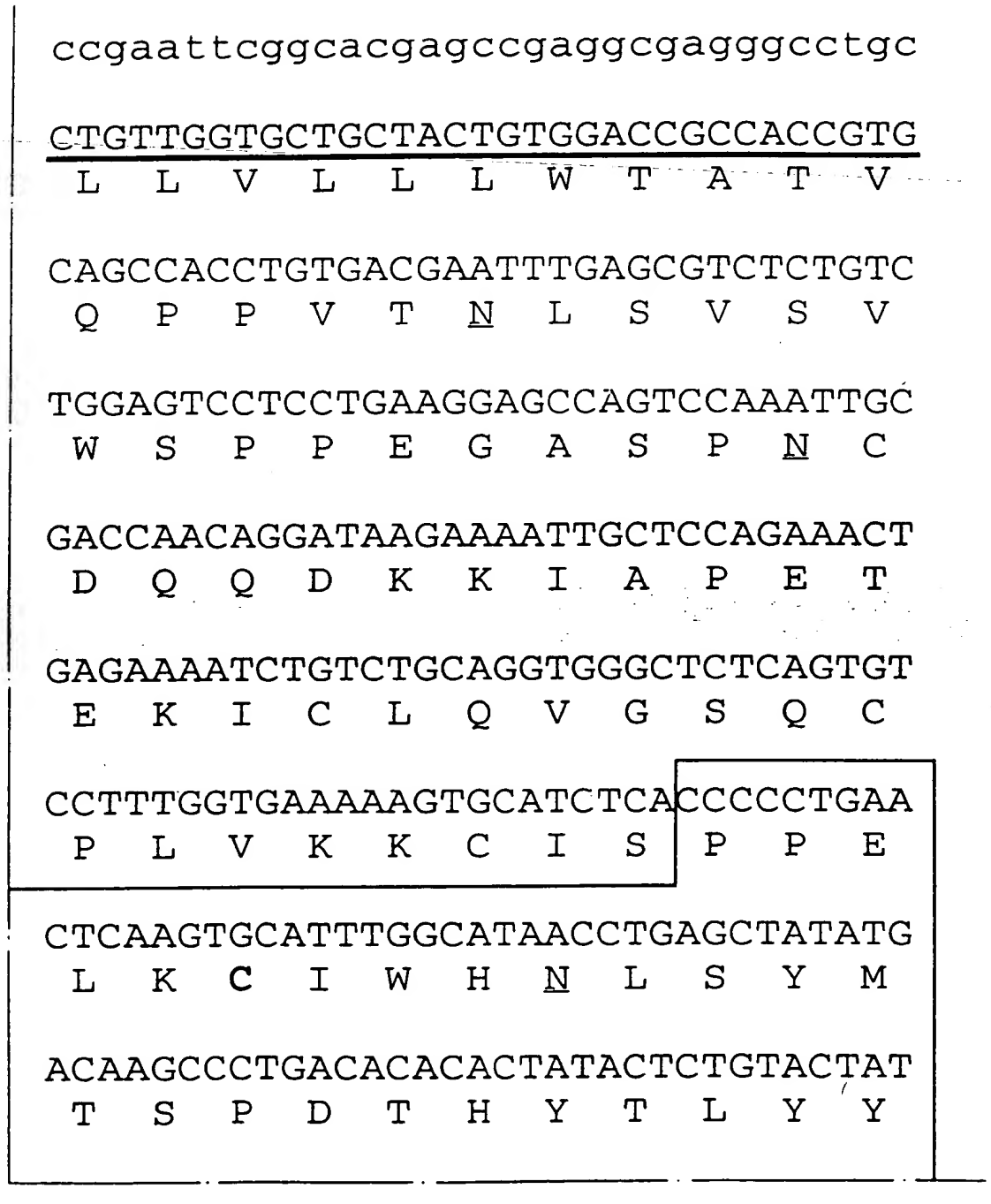


Fig. 1(i)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L L V L L L W T A T V
CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q P P V T N L S V S V
TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W S P P E G A S P N C
GACCAACAGGATAAGAAAATTGCTCCAGAAACT
D Q Q D K K I A P E T
GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C
CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P L V K K C I S P P E
CTCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M
ACAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Fig. 1(ii)

481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTCCTTTAAATTGACTAAA
181	I A **C** S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L **W** **S** **D** **W** **S** E

Fig. 1(iii)

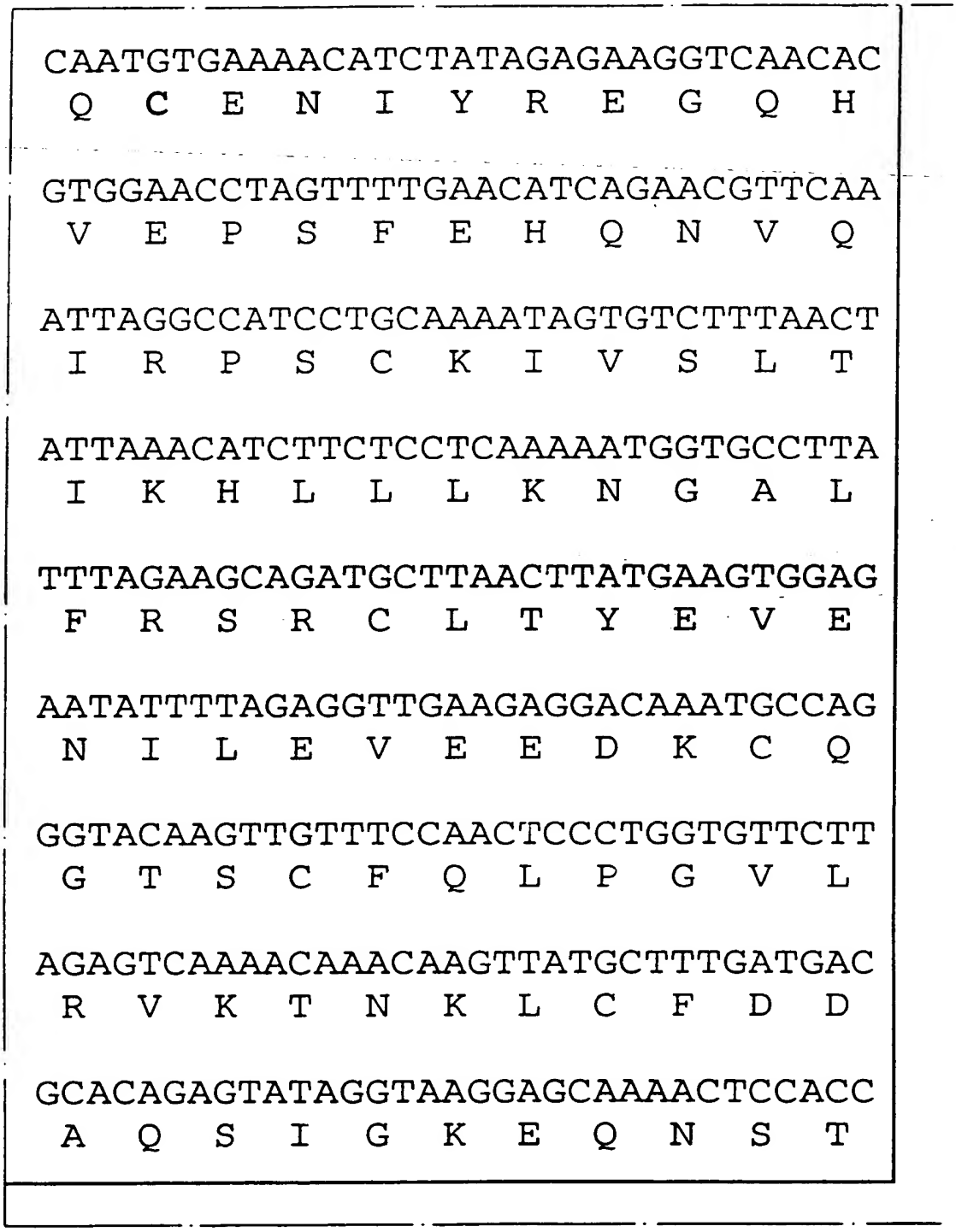

Fig. 1(iv)

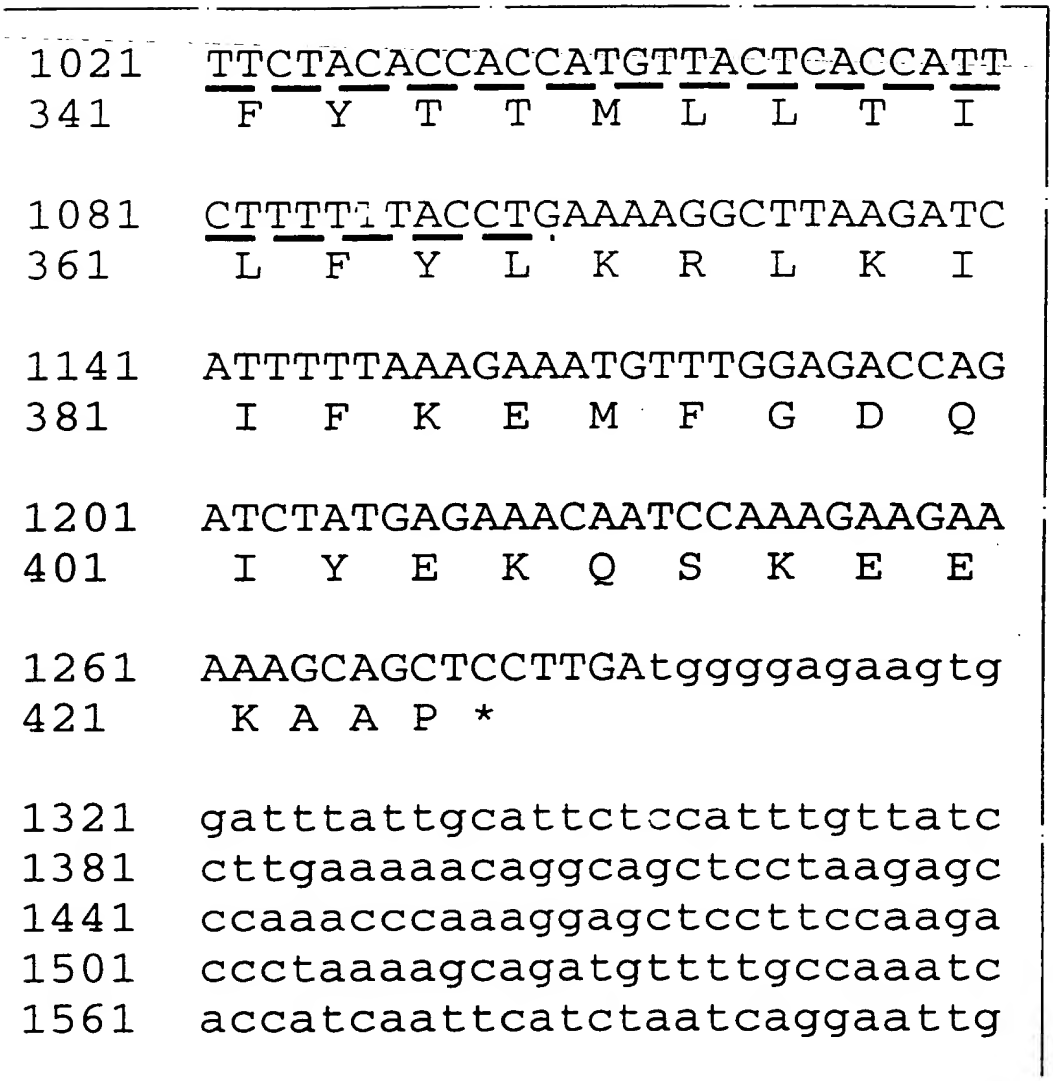

Fig. 1(v)

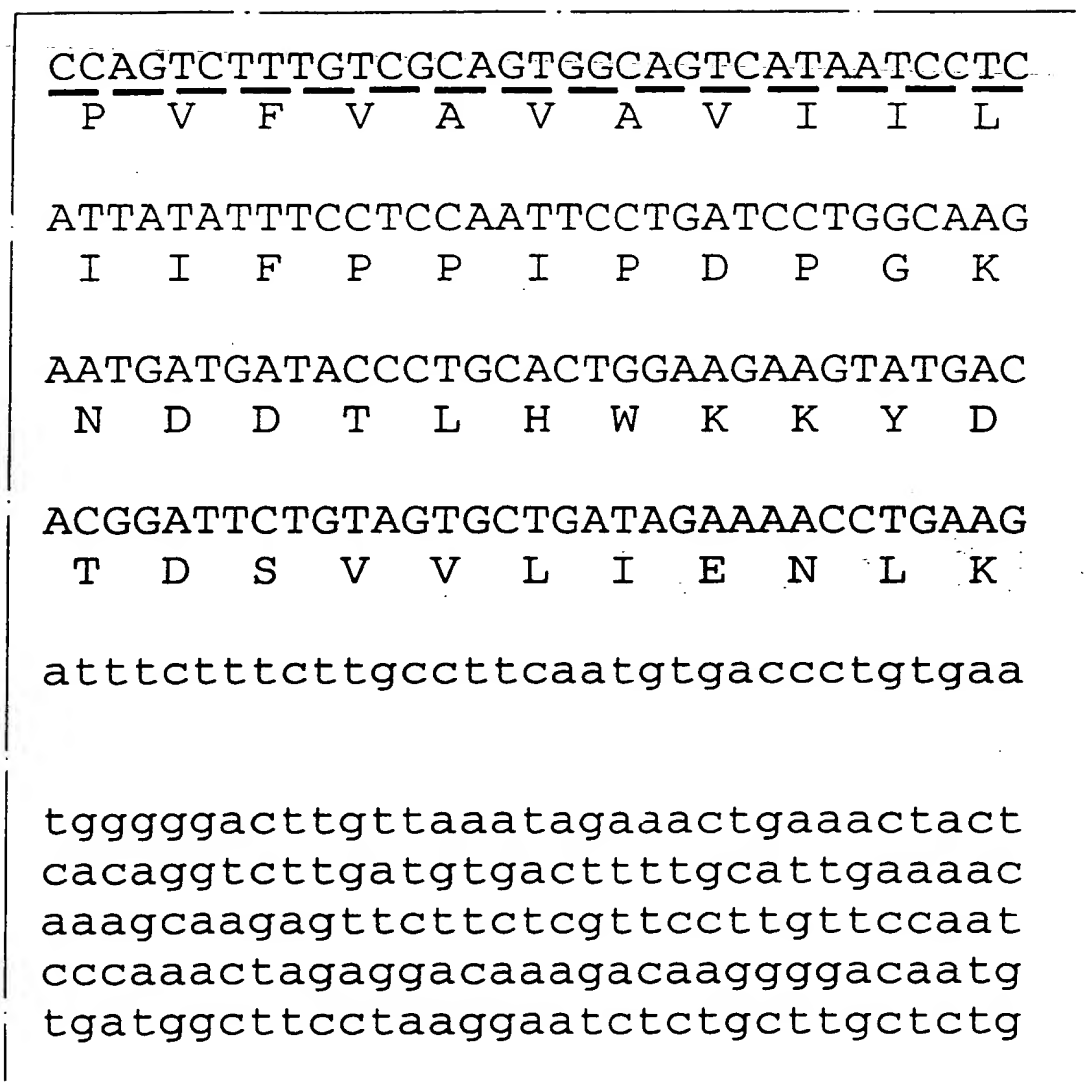

Fig. 1(vi)

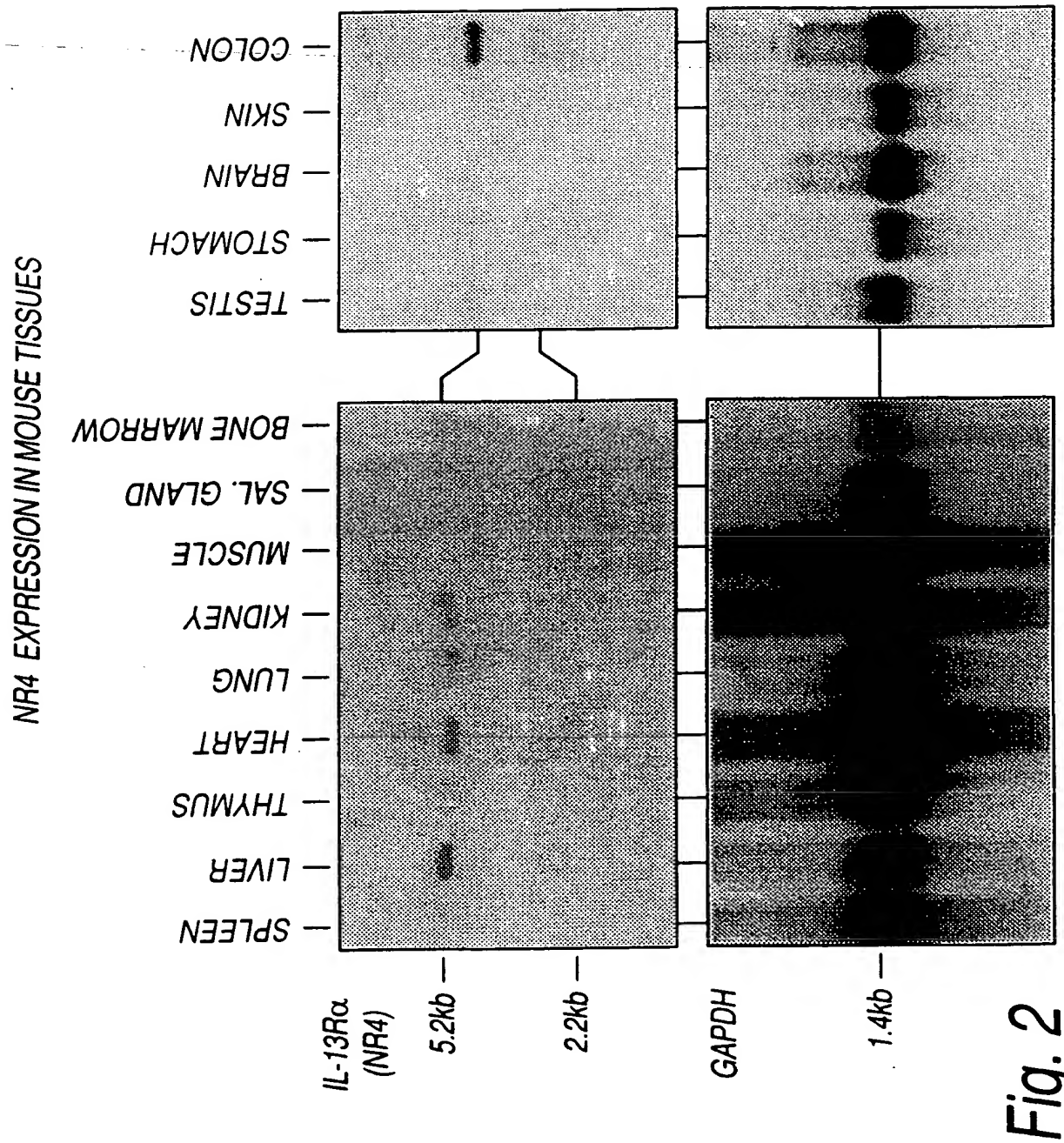
NR4 EXPRESSION IN MOUSE TISSUES
COLON
SKIN
BRAIN
STOMACH
TESTIS
BONE MARROW
SAL. GLAND
MUSCLE
KIDNEY
LUNG
HEART
THYMUS
LIVER
SPLEEN
IL-13Rα (NR4)
5.2kb
2.2kb
GAPDH
1.4kb

Fig. 2

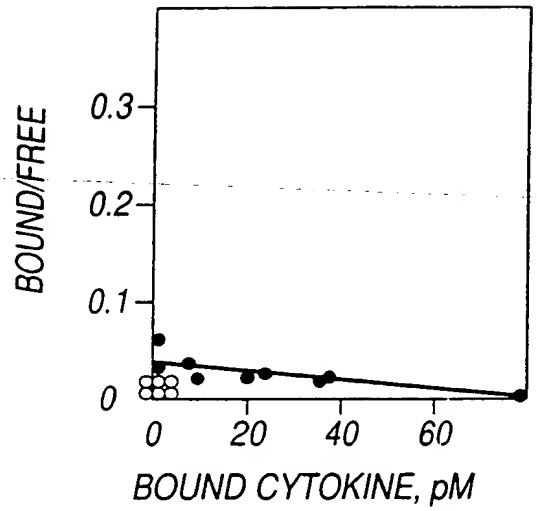

Fig. 3(A)

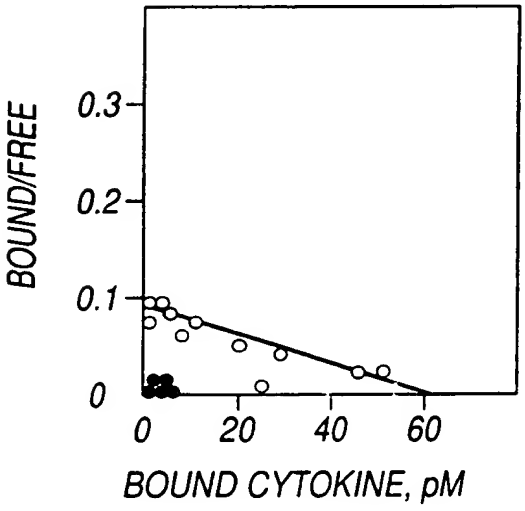

Fig. 3(B)

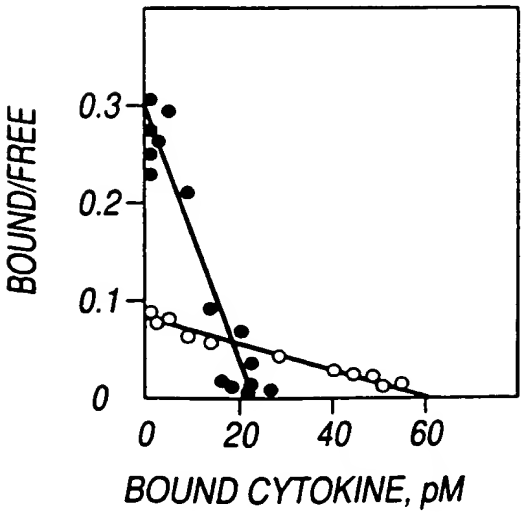

Fig. 3(C)

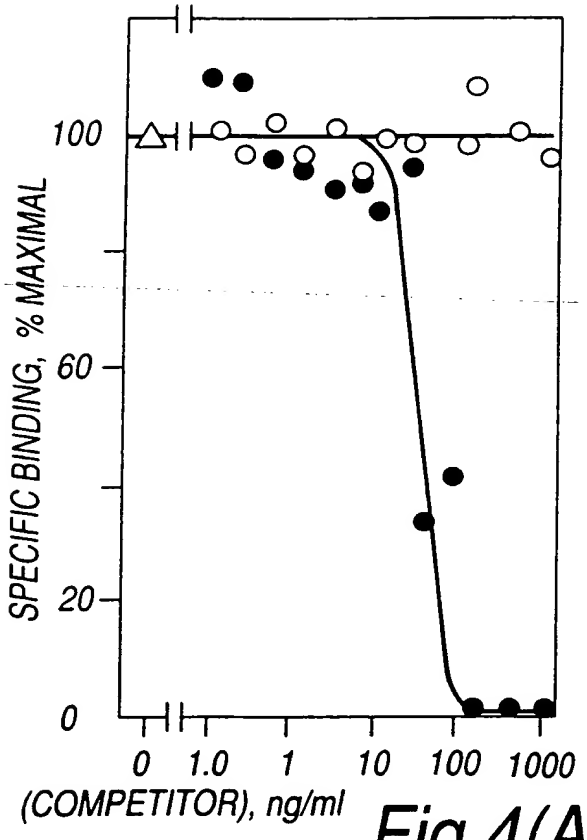

Fig.4(A)

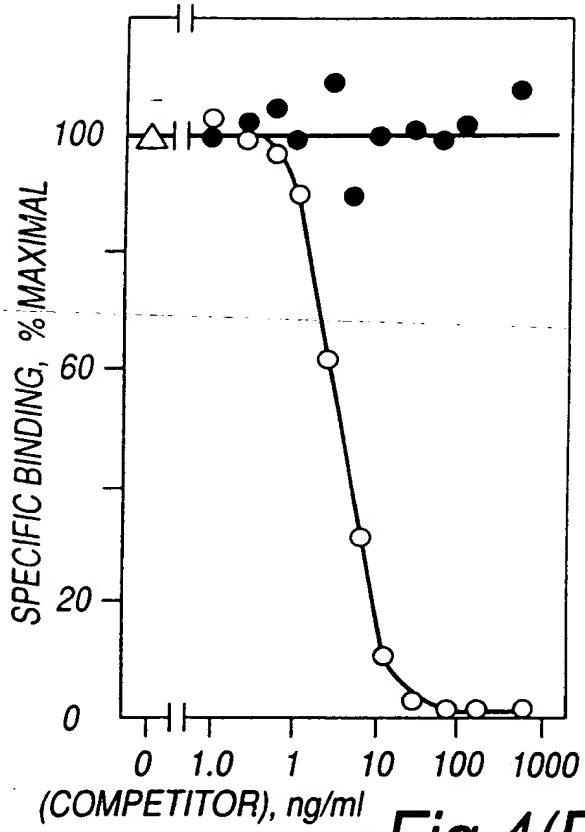

Fig.4(B)

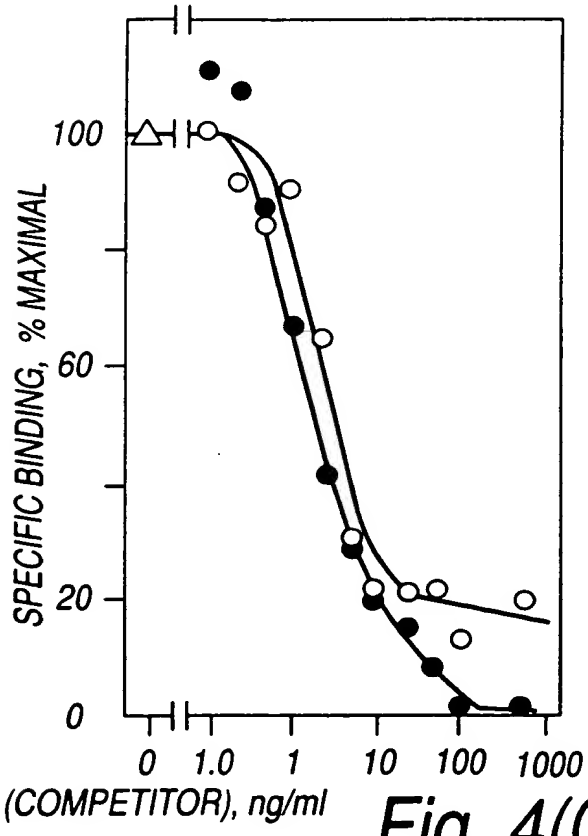

Fig. 4(C)

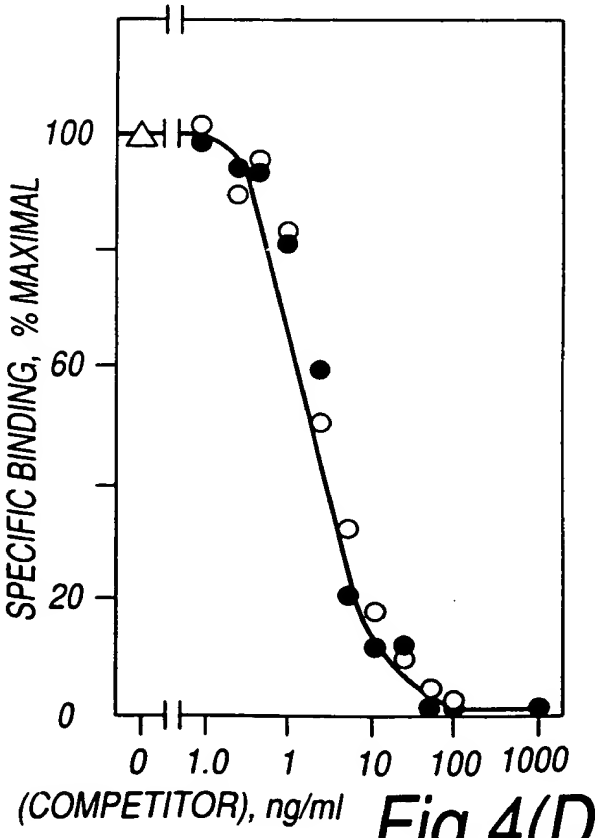

Fig.4(D)

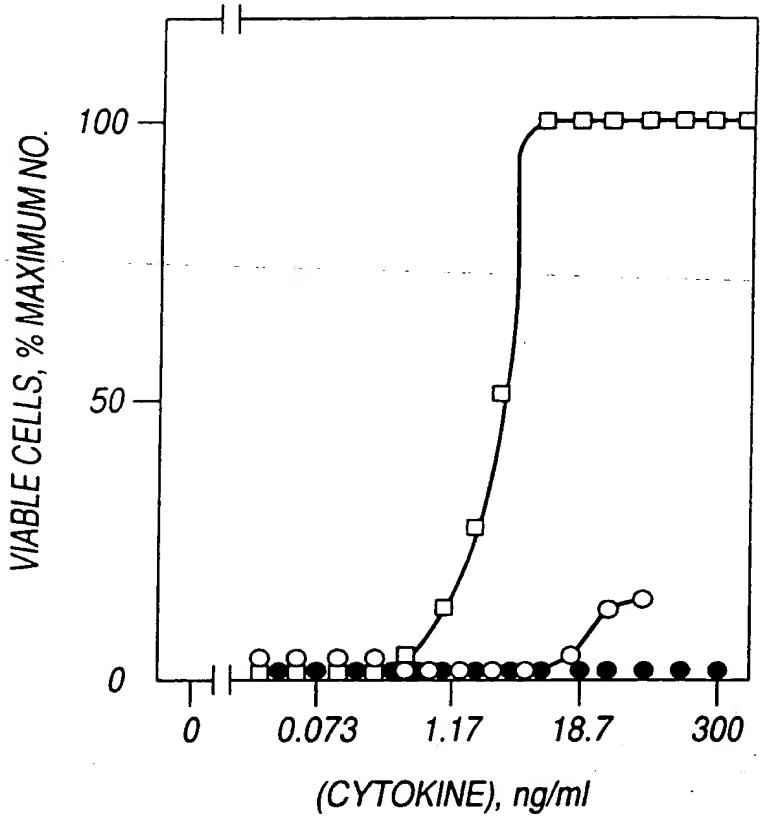
100
50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300
(CYTOKINE), ng/ml

Fig. 5(A)

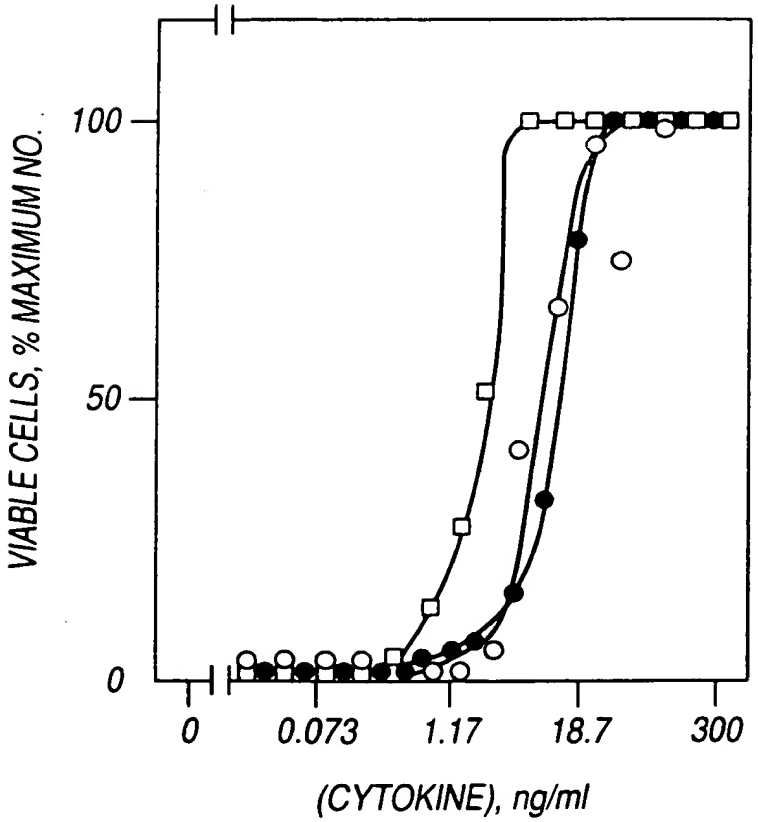
100
50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300
(CYTOKINE), ng/ml

Fig. 5(B)

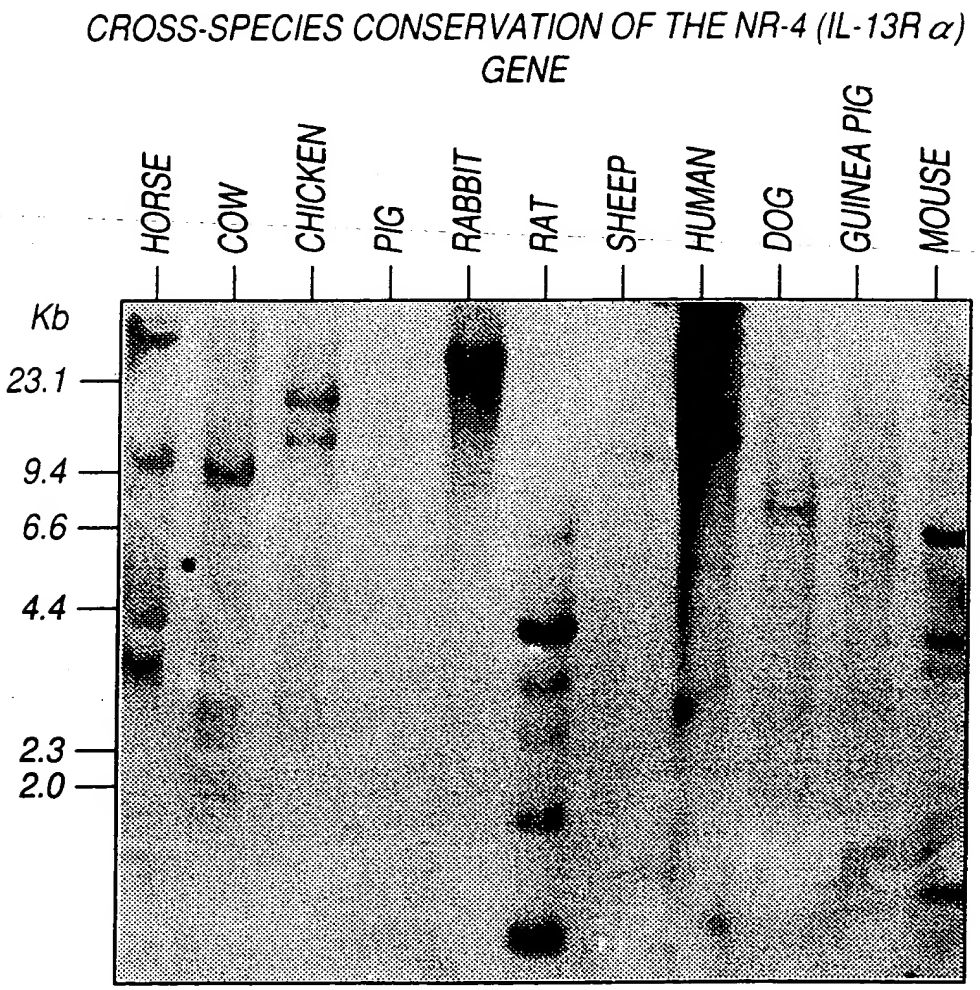

Fig. 6

(major)

DYKDD DDYKD DDESR TEVQP PVTXL SV
1 5 10 15 20 25

(minor)

ASISS SDYKD DDESR TEVQP PVTXL SV
1 5 10 15 20 25

Fig. 10

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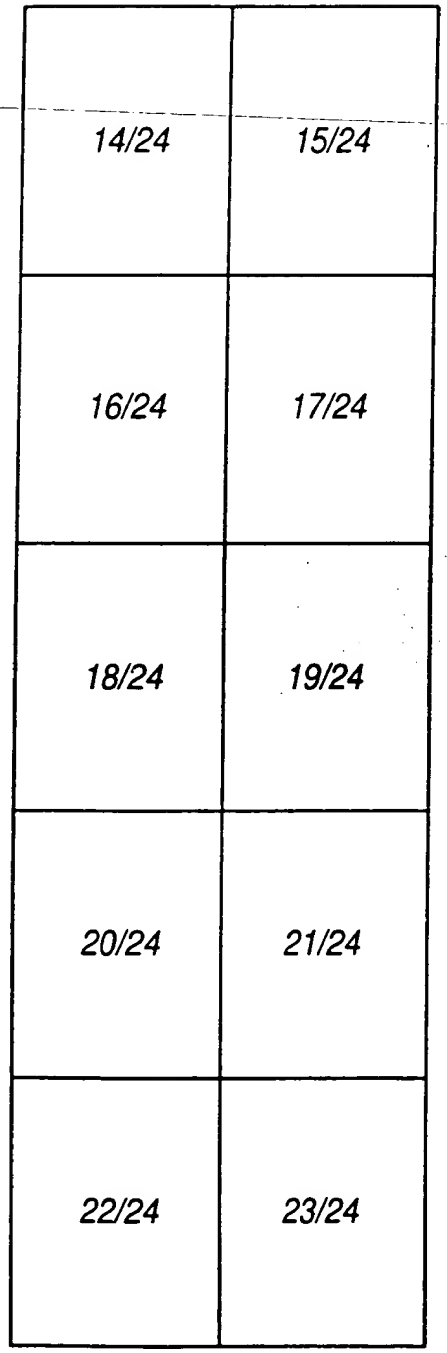
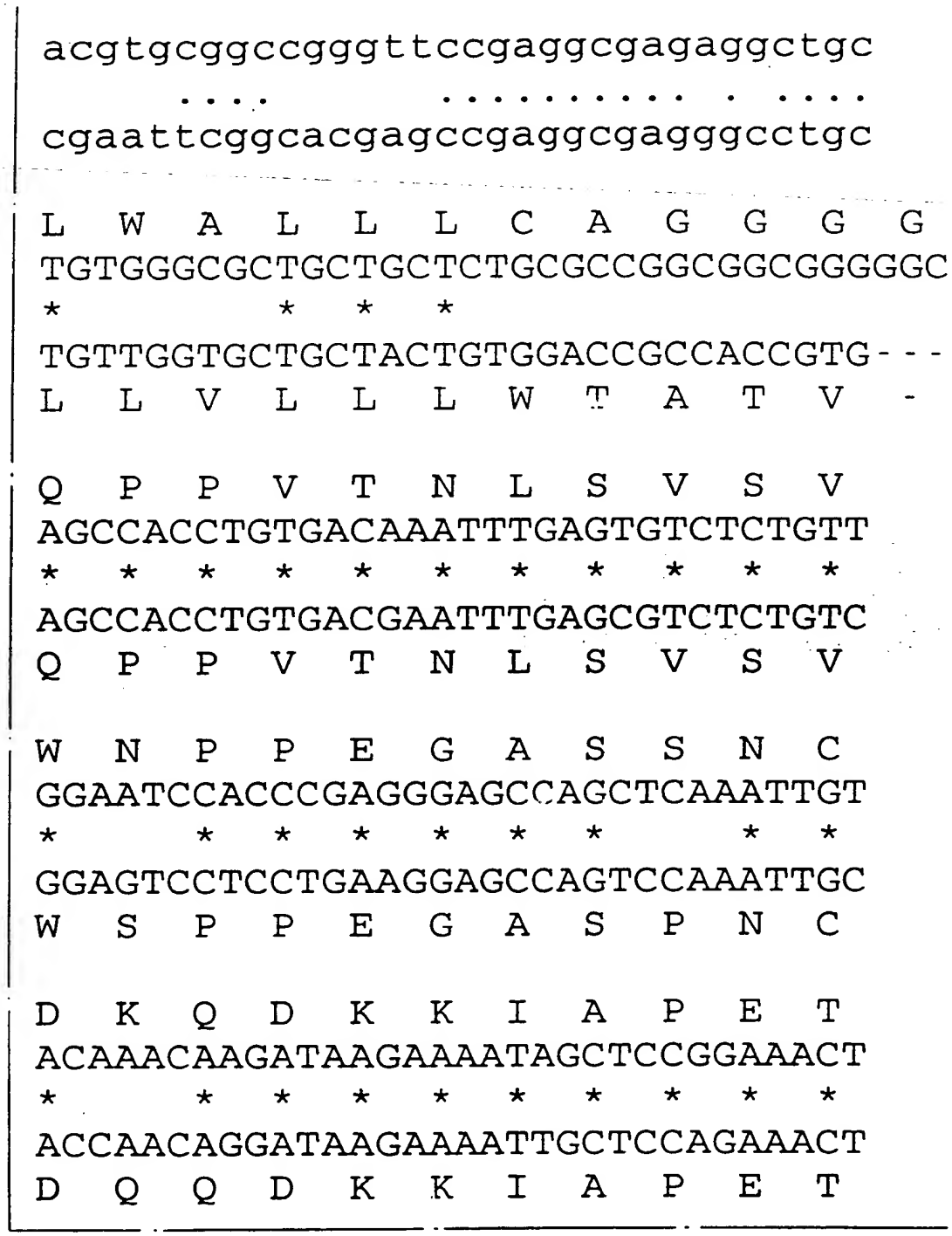


Fig. 7

```
H          gagtctaacacggaccaaggagtttaac

M   -60    tgaaaagatagaataaatggcctcgtgc

H            M   E   W   P   A   R   L   C   G
           ATGGAGTGGCCGGCGCGGCTCTGCGGGC
             *           *   *       *
M   1      ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M   1        M   A   R   P   A   L   L   G   E

H            G   G   G   G   A   P   T   E   T
H          GGGGGCGGGGGCGCGCCTACGGAAACTC
             *               *       *   *
M   61     GGCCAAGTTGCCGCGGCCACAGAAGTTC
M   21       G   Q   V   A   A   A   T   E   V

H            E   N   L   C   T   V   I   W   T
H          GAAAACCTCTGCACAGTAATATGGACAT
             *   *   *   *   *       *   *   *
M   121    GAAAATCTCTGCACGATAATATGGACGT
M   41       E   N   L   C   T   I   I   W   T

H            S   L   W   Y   F   S   H   F   G
H          AGTCTATGGTATTTTAGTCATTTTGGCG
               *       *   *   *   *   *
M   181    ACTCTCAGATATTTTAGTCACTTTGATG
M   61       T   L   R   Y   F   S   H   F   D
```

Fig. 7(i)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cgaattcggcacgagccgaggcgagggcctgc
L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---
L L V L L L W T A T V -
Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q P P V T N L S V S V
W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W S P P E G A S P N C
D K Q D K K I A P E T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D Q Q D K K I A P E T

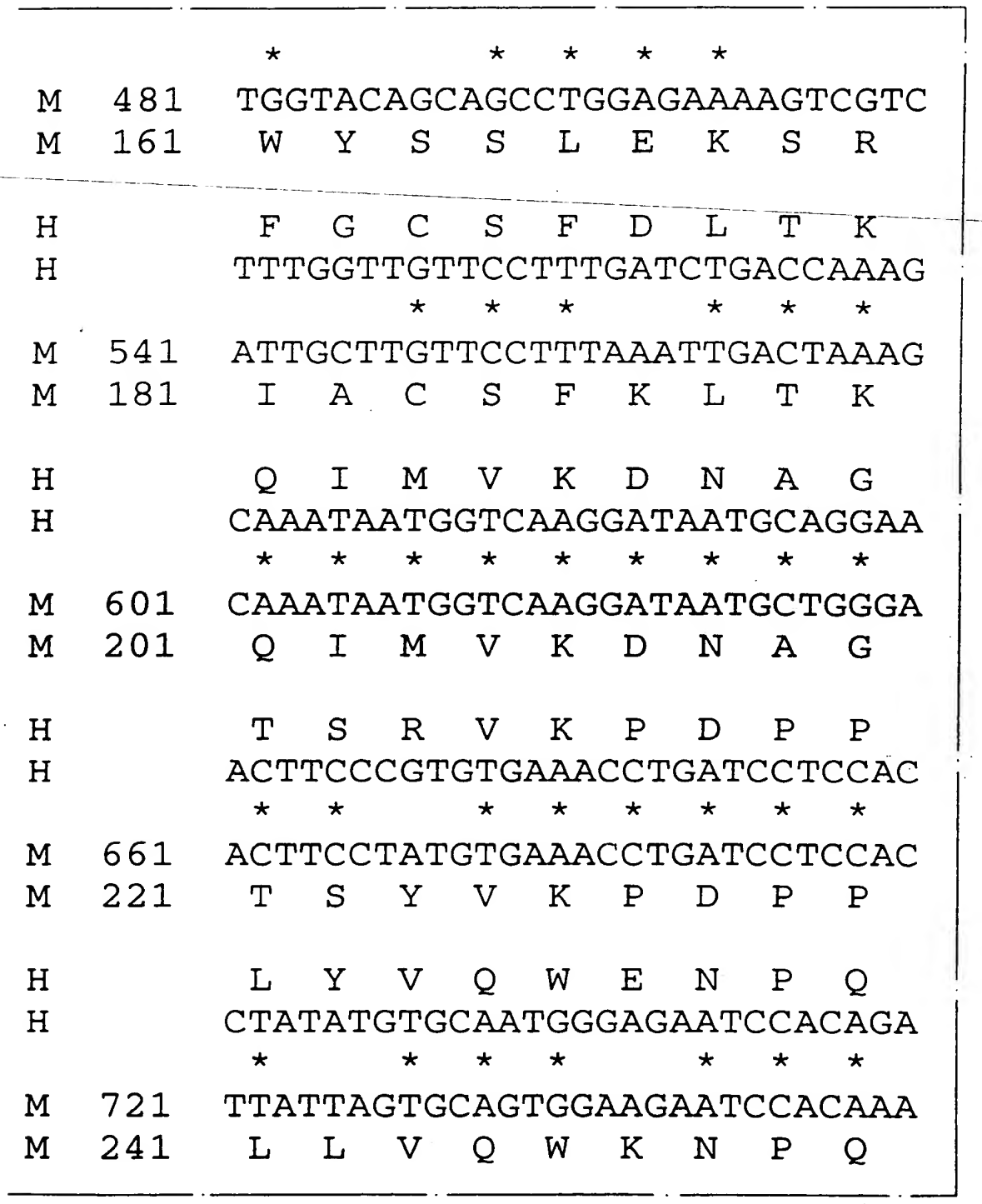
Fig. 7(ii)

```
H          R  R  S  I  E  V  P  L  N
H          CGTCGTTCAATAGAAGTACCCCTGAATG
                 *        *     *  *
M  241     CATCGTAAAGAGGAATTACCCCTGGATG
M  81       H  R  K  E  E  L  P  L  D

H          S  T  N  E  S  E  K  P  S
H          AGCACCAATGAGAGTGAGAAGCCTAGCA
           *     *  *  *  *  *  *  *
M  301     AGTGCCAATGAAAGTGAGAAGCCTAGCC
M  101      S  A  N  E  S  E  K  P  S

H          G  D  P  E  S  A  V  T  E
H          GGTGATCCTGAGTCTGCTGTGACTGAAC
           *  *  *  *  *  *  *  *  *
M  361     GGTGATCCTGAGTCCGCTGTGACTGAGC
M  121      G  D  P  E  S  A  V  T  E

H          K  C  S  W  L  P  G  R  N
H          AAGTGTTCTTGGCTCCCTGGAAGGAATA
           *  *  *  *  *  *  *  *  *
M  421     AAGTGTTCCTGGCTCCCTGGAAGGAATA
M  141      K  C  S  W  L  P  G  R  N

H          W  H  R  S  L  E  K  I  H
H          TGGCACAGAAGCCTGGAAAAAATTCATC
```

Fig. 7(iii)

```
E  R  I  C  L  Q  V  G  S  Q  C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
*     *  *  *  *  *  *  *  *  *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E  K  I  C  L  Q  V  G  S  Q  C

I  L  V  E  K  C  I  S  P  P  E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
   *  *  *  *  *  *  *  *  *  *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P  L  V  K  K  C  I  S  P  P  E

L  Q  C  I  W  H  N  L  S  Y  M
TTCAATGCATTTGGCACAACCTGAGCTACATG
*     *  *  *  *  *  *  *  *  *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L  K  C  I  W  H  N  L  S  Y  M

T  S  P  D  T  N  Y  T  L  Y  Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
*  *  *  *  *     *  *  *  *  *
CAAGCCCTGACACACACTATACTCTGTACTAT
T  S  P  D  T  H  Y  T  L  Y  Y

Q  C  E  N  I  F  R  E  G  Q  Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC
```

Fig. 7(iv)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M 161 W Y S S L E K S R
H F G C S F D L T K
H TTTGGTTGTTCCTTTGATCTGACCAAAG
* * * * * *
M 541 ATTGCTTGTTCCTTTAAATTGACTAAAG
M 181 I A C S F K L T K
H Q I M V K D N A G
H CAAATAATGGTCAAGGATAATGCAGGAA
* * * * * * * * *
M 601 CAAATAATGGTCAAGGATAATGCTGGGA
M 201 Q I M V K D N A G
H T S R V K P D P P
H ACTTCCCGTGTGAAACCTGATCCTCCAC
* * * * * * * *
M 661 ACTTCCTATGTGAAACCTGATCCTCCAC
M 221 T S Y V K P D P P
H L Y V Q W E N P Q
H CTATATGTGCAATGGGAGAATCCACAGA
* * * * * * *
M 721 TTATTAGTGCAGTGGAAGAATCCACAAA
M 241 L L V Q W K N P Q

Fig. 7(v)

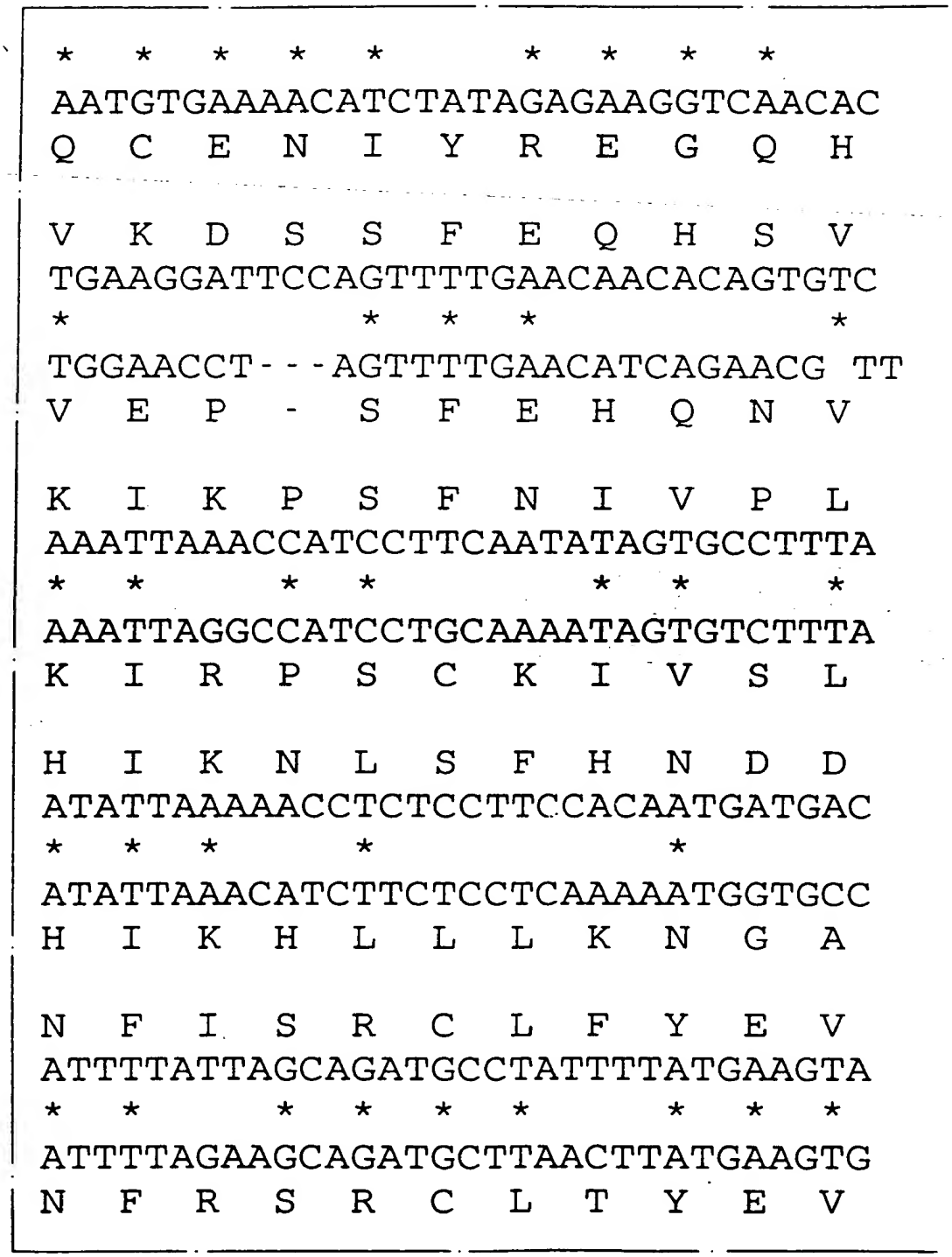
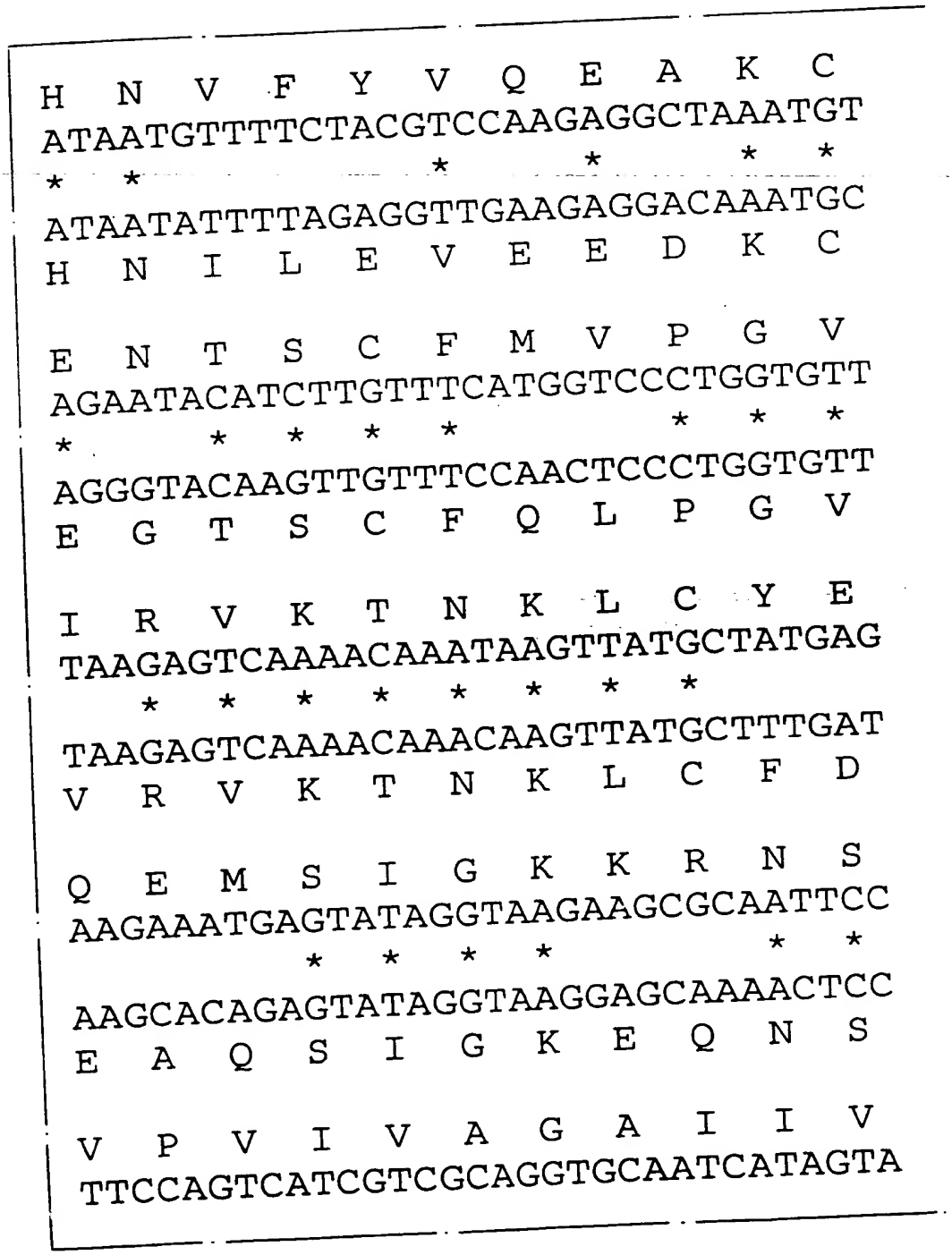

* * * * * * * * *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H
V K D S S F E Q H S V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
* * * *
TGGAACCT---AGTTTTGAACATCAGAACG TT
V E P - S F E H Q N V
K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * * * *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L
H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
* * * * *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A
N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * * * * * *
ATTTTAGAAGCAGATGCTTAACTTATGAAGTG
N F R S R C L T Y E V

Fig. 7(vi)

```
H          E  V  N  N  S  Q  T  E  T
H          GAAGTCAATAACAGCCAAACTGAGACAC
           *  *  *  *     *  *
M   781    GAGGTCAATAATACTCAAACCGACCGAC
M   261    E  V  N  N  T  Q  T  D  R

H          E  N  P  E  F  E  R  N  V
H          GAGAATCCAGAATTTGAGAGAAATGTGG
              *     *        *  *
M   841    CAGAATTCCGAATCTGATAGAAACATGG
M   281    Q  N  S  E  S  D  R  N  M

H          L  P  D  T  L  N  T  V  R
H          CTTCCTGATACTTTGAACACAGTCAGAA
           *     *           *  *  *
M   901    CTTGCCGACGCTGTCTACACAGTCAGAG
M   301    L  A  D  A  V  Y  T  V  R

H          D  D  K  L  W  S  N  W  S
H          GATGACAAACTCTGGAGTAATTGGAGCC
           *     *  *  *  *     *  *
M   961    GACAACAAACTGTGGAGTGATTGGAGTG
M   321    D  N  K  L  W  S  D  W  S

H          T  L  Y  I  T  M  L  L  I
H          ACACTCTACATAACCATGTTACTCATTG
```

Fig. 7(vii)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* * * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C
E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * * * * *
AGGGTACAAGTTGTTTCCAACTCCCTGGTGTT
E G T S C F Q L P G V
I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D
Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S
V P V I V A G A I I V
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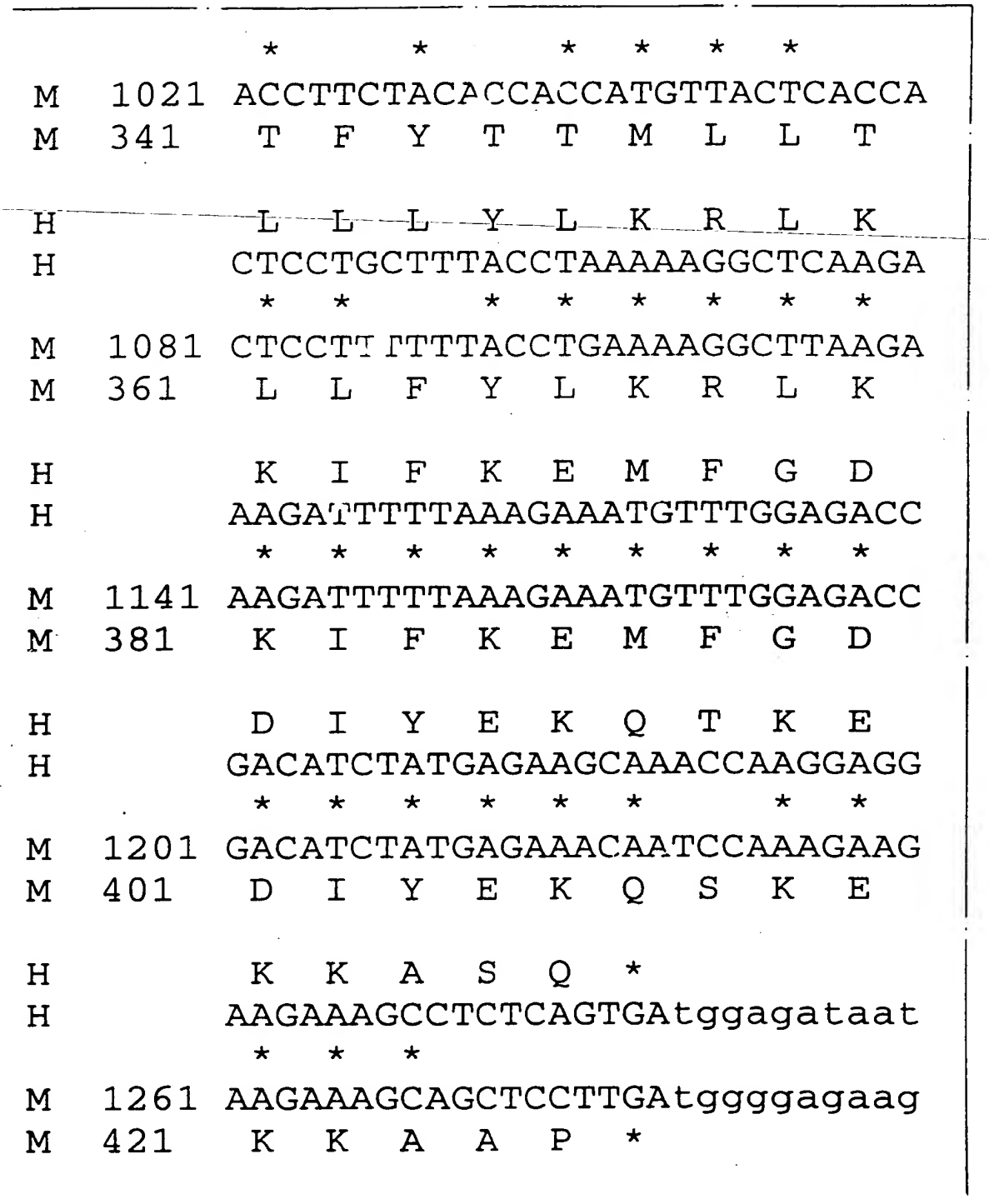
Fig. 7(viii)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M 341 T F Y T T M L L T
H L L L Y L K R L K
H CTCCTGCTTTACCTAAAAAGGCTCAAGA
M 1081 CTCCTTTTTTACCTGAAAAGGCTTAAGA
M 361 L L F Y L K R L K
H K I F K E M F G D
H AAGATTTTTAAAGAAATGTTTGGAGACC
M 1141 AAGATTTTTAAAGAAATGTTTGGAGACC
M 381 K I F K E M F G D
H D I Y E K Q T K E
H GACATCTATGAGAAGCAAACCAAGGAGG
M 1201 GACATCTATGAGAAACAATCCAAAGAAG
M 401 D I Y E K Q S K E
H K K A S Q *
H AAGAAAGCCTCTCAGTGAtggagataat
M 1261 AAGAAAGCAGCTCCTTGAtggggagaag
M 421 K K A A P *

Fig. 7(ix)

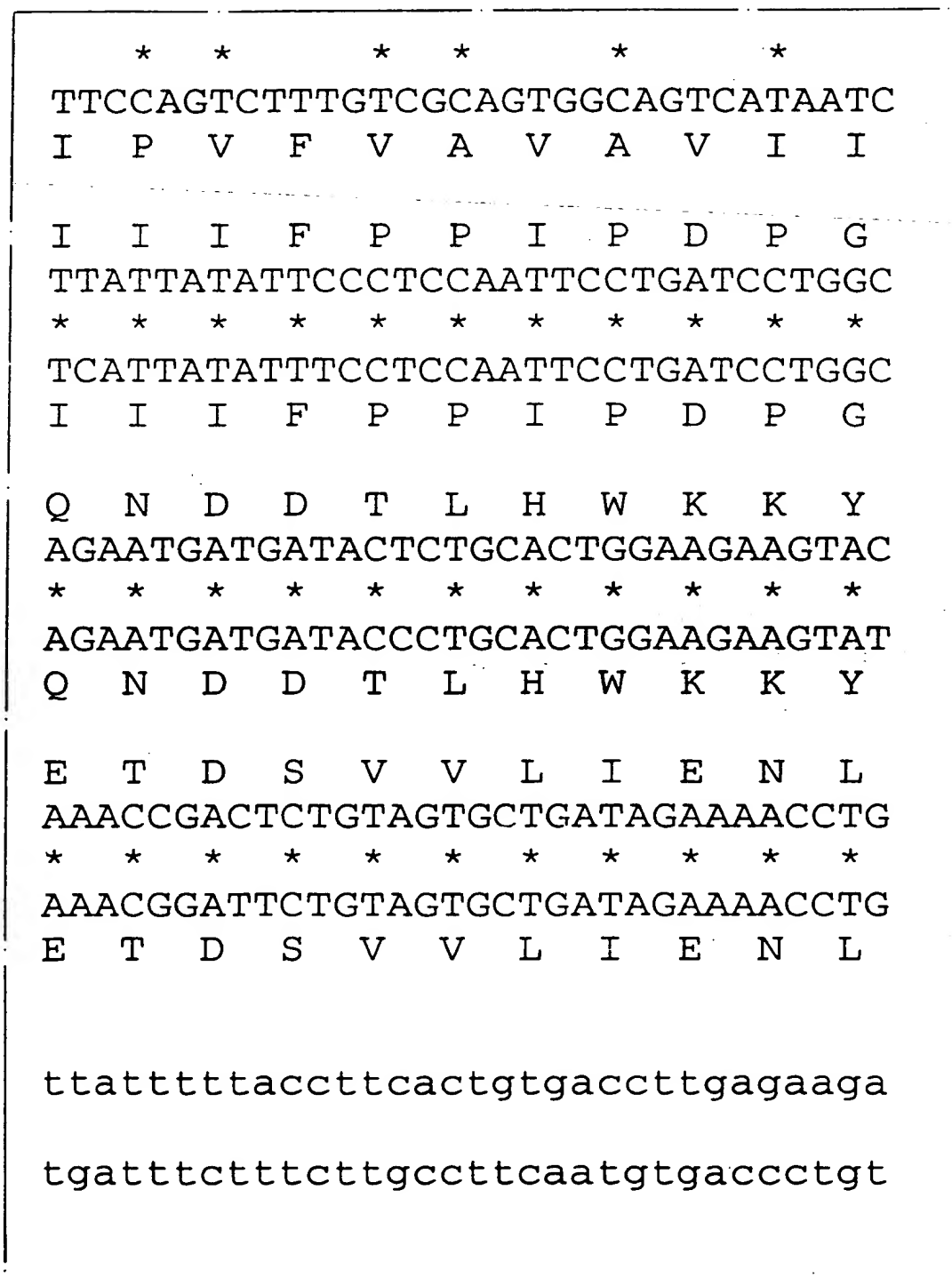

Fig. 7(x)

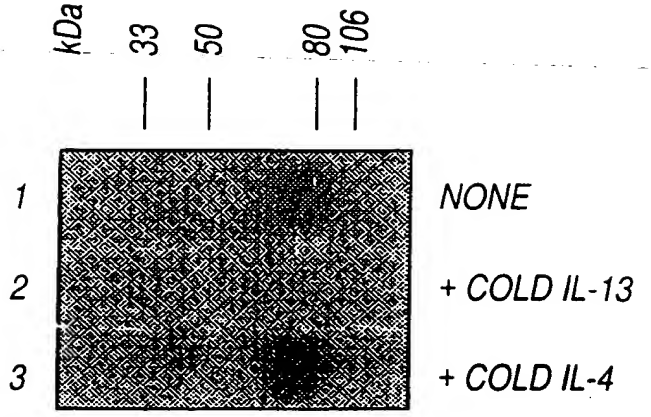

Fig. 8

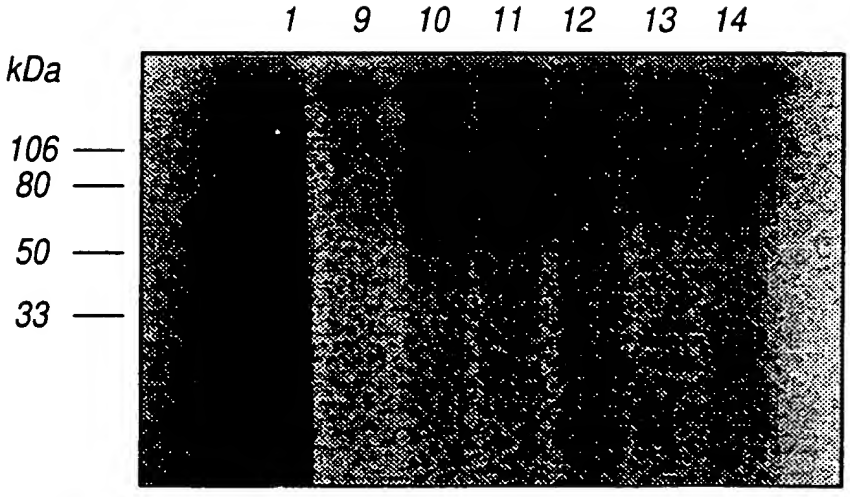

Fig. 9